

Pathway Enrichment

Name	# of Entities	Expanded	Overlap	p-value
Actin Cytoskeleton Regulation	51	539	79	0.000126
Guanylate Cyclase Pathway	36	1219	151	
TGFBR -> ATF/GADD/MAX/TP53 signaling	17	17	7	0.000696
TGFBR -> MEF/MYOD/MYOG signaling	27	27	9	0.000752
EphrinR -> actin signaling	15	216	36	0.00101
Cell Cycle Regulation	135	2164	248	
FrizzledR -> JUN/PAX2 signaling	16	28	8	0.004396
NGFR -> MEF signaling	23	23	7	0.005198
EndothelinRb -> AP-1/CREB/ELK-SRF signaling	51	104	19	0.005591
EDG3/5 -> AP-1/ELK-SRF signaling	41	91	17	0.006791
CXCR4 -> STAT signaling	9	9	4	0.007821
FGFR3 -> STAT signaling	14	14	5	0.008554
TNFRSF6 -> DDIT3 signaling	14	14	5	0.008554
Focal Adhesion Regulation	41	308	43	0.010808
FibronectinR -> AP-1/ELK-SRF/SREBF signaling	40	74	14	0.011987
TGFBR -> AP-1 signaling	16	16	5	0.015817
TNFRSF5/6 -> RB1/E2F signaling	16	16	5	0.015817
PTAFR -> AP-1/ATF1/CREB/ERK-SRF signaling	44	107	18	0.015955
Hedgehog Pathway	17	624	77	0.018346
Notch Pathway	40	1486	167	
GHR -> STAT signaling	12	12	4	0.024193
IL6ST -> STAT5B signaling	7	7	3	0.024546
SerotoninR4/6/7 -> NR3C signaling	24	44	9	0.025117
FSHR -> CREB/ELK-SRF/GATA4 signaling	29	81	14	0.025328
TGFBR -> CREB/ELK-SRF signaling	18	18	5	0.026321
VIPR -> CREB/CEBP signaling	31	68	12	0.031829
Nicotinate and nicotinamide metabolism	46	116	9	0.032099
IL1R -> STAT3 signaling	13	13	4	0.03229
FGFR1 -> STAT signaling	13	13	4	0.03229
CannabinoidR -> AP-1/EGR signaling	51	134	20	0.037754
TGFBR/BMPR -> SMAD2/3 signaling	14	14	4	0.041784
ICAM1 -> AP-1/CREB/ELK-SRF signaling	29	48	9	0.04187
ProstaglandinIR -> ATF1/ELK-SRF/CREB signaling	35	71	12	0.042782
GlucagonR -> CREB/ELK-SRF/SP1 signaling	20	41	8	0.043494
TNFRSF1A -> CREB/ELK-SRF signaling	32	41	8	0.043494
NCAM1 -> CREB/ELK-SRF/MYC signaling	17	27	6	0.0437

GO Analysis

Annotation	Total Genes	Genome	p-value
protein transport	83	548	1.99E-12
positive regulation of transcription from RNA polymerase II promoter	64	376	4.41E-12
chromatin modification	37	183	1.22E-09
negative regulation of transcription	32	158	1.51E-08
regulation of transcription from RNA polymerase II promoter	42	251	3.50E-08
positive regulation of transcription, DNA-dependent	28	136	8.21E-08
negative regulation of transcription from RNA polymerase II promoter	45	290	1.15E-07
mRNA splice site selection	8	12	1.55E-07
Wnt receptor signaling pathway	26	128	3.12E-07
small GTPase mediated signal transduction	39	259	1.71E-06
intracellular protein transport	35	226	3.00E-06
germ cell development	12	37	3.02E-06
protein import into nucleus, docking	8	18	9.53E-06
G1-S transition of mitotic cell cycle	14	55	1.12E-05
mRNA processing	38	270	1.16E-05
mRNA transport	16	70	1.20E-05
anti-apoptosis	30	194	1.53E-05
protein amino acid methylation	7	15	2.39E-05
positive regulation of apoptosis	24	142	2.42E-05
interspecies interaction between organisms	33	229	2.63E-05
positive regulation of transcription	25	152	2.67E-05
apoptosis	61	531	2.69E-05
cell cycle	61	532	2.85E-05
visual learning	10	33	3.95E-05
RNA splicing	33	234	4.08E-05
protein amino acid dephosphorylation	24	149	5.42E-05
protein amino acid autophosphorylation	18	97	7.03E-05
cell cycle arrest	20	115	7.43E-05

muscle contraction	17	89	7.60E-05
positive regulation of protein amino acid phosphorylation	10	36	9.02E-05
cell proliferation	44	362	9.59E-05
response to hypoxia	27	184	0.000101
protein amino acid phosphorylation	75	723	0.000108
in utero embryonic development	26	175	0.000109
multicellular organismal development	102	1061	0.000137
regulation of transcription	58	528	0.000145
positive regulation of gene-specific transcription	7	19	0.000147
endocytosis	22	140	0.000158
negative regulation of cell growth	16	86	0.000169
regulation of heart contraction	10	41	0.000293
positive regulation of anti-apoptosis	9	34	0.000302
mRNA export from nucleus	7	21	0.000302
transcription from RNA polymerase II promoter	23	157	0.000326
heart development	24	168	0.000359
anatomical structure morphogenesis	18	110	0.000365
regulation of cell proliferation	19	121	0.000435
liver development	13	67	0.000441
positive regulation of cell proliferation	38	321	0.000469
actin cytoskeleton organization	23	161	0.000471
negative regulation of transcription, DNA-dependent	17	103	0.000474
nuclear mRNA splicing, via spliceosome	19	122	0.000483
synaptic transmission	27	204	0.000551
blood vessel morphogenesis	6	17	0.000584
nucleocytoplasmic transport	8	30	0.000618
cell migration	14	78	0.000618
nervous system development	45	409	0.000741
neural crest cell migration	7	24	0.000753
palate development	8	31	0.000785
modification-dependent protein catabolic process	52	498	0.001009
regulation of Rho protein signal transduction	14	82	0.001034
S-adenosylmethionine metabolic process	3	4	0.001142
N-terminal protein amino acid acetylation	3	4	0.001142
isocitrate metabolic process	3	4	0.001142
negative regulation of cell proliferation	36	315	0.001234
barbed-end actin filament capping	7	26	0.001272
negative regulation of apoptosis	23	174	0.00139
viral genome replication	5	14	0.001614
chromatin assembly or disassembly	11	59	0.001674
heart looping	7	28	0.002035
lung development	15	98	0.002175
response to hormone stimulus	11	61	0.002212
regulation of G-protein coupled receptor protein signaling pathway	8	36	0.002233
protein import into nucleus	8	36	0.002233
protein export from nucleus	5	15	0.002288
N-acetylglucosamine metabolic process	5	15	0.002288
transmembrane receptor protein tyrosine kinase signaling pathway	15	99	0.002409
dephosphorylation	15	100	0.002662
negative regulation of cytokine-mediated signaling pathway	3	5	0.002713
negative regulation of lipid transport	3	5	0.002713
positive regulation of cyclin-dependent protein kinase activity	3	5	0.002713
positive regulation of gluconeogenesis	3	5	0.002713
regulation of transcription from RNA polymerase II promoter in respon	3	5	0.002713
growth hormone receptor signaling pathway	3	5	0.002713
aspartate transport	3	5	0.002713
protein kinase cascade	16	111	0.002954
limb development	4	10	0.003044
cellular response to insulin stimulus	9	46	0.003071
histone methylation	5	16	0.003146
chondrocyte differentiation	5	16	0.003146
negative regulation of neuron apoptosis	11	64	0.003274
regulation of cell shape	11	65	0.003708
skeletal muscle tissue development	11	65	0.003708
intracellular protein transmembrane transport	12	75	0.004016
muscle maintenance	5	17	0.004213
positive regulation of glucose import	6	24	0.004238
loss of chromatin silencing	2	2	0.004491
negative regulation of pinocytosis	2	2	0.004491